

SEQUENCE LISTING

<110> Kaia Palm
Tonis Timmusk
CeMines Research

<120> MAMMALIAN NEURALIZED FAMILY OF
TRANSCRIPTION REGULATORS AND USES THEREFOR

<130> CEMRES.001A

<160> 48

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo sapien

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<211> 574

<212> PRT

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 Cys Pro Pro Thr Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu
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 Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His
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 Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser

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Leu	Thr	Arg	Gly	Val	Gln	Leu	Leu	Asp	Ser	Glu	Leu	Val	Leu	Pro	Asp		
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Cys	Leu	Arg	Pro	Arg	Ser	Phe	Thr	Ala	Leu	Arg	Arg	Pro	Ser	Leu	Arg		
225				230					235					240			
Cys	Glu	Ala	Asp	Glu	Ala	Arg	Leu	Ser	Val	Ser	Leu	Cys	Asp	Leu	Asn		
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Val	Pro	Gly	Ala	Asp	Gly	Asp	Asp	Gly	Ala	Pro	Pro	Ala	Gly	Cys	Pro		
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385				390					395					400			
Leu	Val	Val	Asn	Ala	Asp	Gly	Glu	Leu	His	Leu	Ser	His	Asn	Gly	Ala		
			405						410						415		
Ala	Ala	Gly	Met	Gln	Leu	Cys	Val	Asp	Ala	Ser	Gln	Pro	Leu	Trp	Met		
			420						425						430		
Leu	Phe	Ser	Leu	His	Gly	Ala	Ile	Thr	Gln	Val	Arg	Ile	Leu	Gly	Ser		
			435						440						445		
Thr	Ile	Met	Thr	Glu	Arg	Gly	Gly	Pro	Ser	Leu	Pro	Cys	Ser	Pro	Ala		
			450						455						460		
Ser	Thr	Pro	Thr	Ser	Pro	Ser	Ala	Leu	Gly	Ile	Arg	Leu	Ser	Asp	Pro		
465				470					475					480			
Leu	Leu	Ser	Thr	Cys	Gly	Ser	Gly	Pro	Leu	Gly	Gly	Ser	Ala	Gly	Gly		
			485						490						495		
Thr	Ala	Pro	Asn	Ser	Pro	Val	S										

Val	Asp	Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met	Cys	Leu	Cys	Tyr	Ser
530						535					540				
Cys	Gly	Leu	Arg	Leu	Lys	Lys	Ala	Leu	His	Ala	Cys	Cys	Pro	Ile	Cys
545					550					555					560
Arg	Arg	Pro	Ile	Lys	Asp	Ile	Ile	Lys	Thr	Tyr	Arg	Ser	Ser		
				565					570						

<210> 9
 <211> 1698
 <212> DNA
 <213> mouse

<400> 9

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ctcccggcca	cgcgctgct	cttccacccc	cacactaagg	gctcccagat	cctcatggac	180
ctcagccaca	aggccgtcaa	gaggcaggcc	agcttctgca	atgccatcac	cttcagtaac	240
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gtcttctacc	ggatcaatga	gtcagctgct	atgcttttct	tcagtgggggt	ccggacggtg	540
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agcgagctgg	tgctgcccga	ctgcctgcgg	ccgcgctcct	tcaccgcgct	gcggcgcccg	660
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gcagagcccc	acctgcac					1698

<210> 10
 <211> 557
 <212> PRT
 <213> mouse

<400> 10

Met	Gly	Gly	Gln	Ile	Thr	Arg	Asn	Thr	Ile	His	Asp	Ser	Ile	Gly	Gly
1				5				10						15	
Ser	Phe	Pro	Val	Pro	Ser	His	Arg	Cys	His	His	Lys	Gln	Lys	His	Cys
			20					25					30		
Pro	Pro	Thr	Leu	Ser	Gly	Gly	Gly	Leu	Pro	Ala	Thr	Pro	Leu	Leu	Phe

Ala Pro Asn Ser Pro Val Ser Leu Pro Glu Ser Pro Val Thr Pro Gly
485 490 495
Leu Gly Gln Trp Ser Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val
500 505 510
Asp Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys
515 520 525
Gly Leu Arg Leu Lys Lys Ala Leu His Ala Cys Cys Pro Ile Cys Arg
530 535 540
Arg Pro Ile Lys Asp Ile Ile Lys Thr Tyr Arg Ser Ser
545 550 555

<210> 11
<211> 1035
<212> DNA
<213> mouse

<400> 11
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cgatgccatc acaagcagaa gcattgcccg cctacgctgt caggtggggg gctcccggcc 180
acgccgctgc tcttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240
aaggccgtca agaggcaggc cagcttctgc aatgccatca ccttcagtaa ccgcccgggtg 300
ctcatctacg agcaagtcag gctgaagatc accaagaagc aatgctgctg gagcggggcc 360
ctgcgacttg gcttcaccag caaggaccct tcccgcatcc accccgactc gctgcccag 420
tacgctgcc ctgacctggt gtctcagagt ggcttctggg ccaaagcatt gcctgaggag 480
tttgccaacg agggcaacat cattgccttc tgggtggaca agaagggccg cgtcttctac 540
cggatcaatg agtcagctgc tatgcttttc ttcagtgggg tccggacggt ggacccgctc 600
tgggcccctg tggacgtcta cggcctcacg cgggggtgtc agctgctagg ctccaccatc 660
atgactgaac ggggtggccc atctctcccc tgcacactg cttccactcc aacctacccc 720
agtgcctggt gcatccgctt gtctgacccc ttgctcagca cctgcggttc tgggccccta 780
gggtggtctg ctggaggggac agcccccaat tcacctgtga gcctgcccga gtcaccggtg 840
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acagtcattc acacgtgtgg ccacatgtgc ctgtgtact cctgtggcct gcgcctcaag 960
aaggccctgc acgctgtctg ccccatctgc cgtcgcccca tcaaggacat catcaagacc 1020
taccgcagct cgtag 1035

<210> 12
<211> 344
<212> PRT
<213> mouse

<400> 12
Met Gly Asn Asn Phe Ser Ser Val Ser Ser Leu Gln Arg Gly Asn Pro
1 5 10 15
Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Glu Ser Ile Gly
20 25 30
Gly Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His
35 40 45
Cys Pro Pro Thr Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu
50 55 60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His
65 70 75 80
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser
85 90 95

<210> 14
 <211> 291
 <212> PRT
 <213> mouse

<400> 14

Met	Gly	Asn	Asn	Phe	Ser	Ser	Val	Ser	Ser	Leu	Gln	Arg	Gly	Asn	Pro
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Ser	Arg	Ala	Ser	Arg	Gly	His	Pro	Gln	Asn	Leu	Lys	Glu	Ser	Ile	Gly
		20						25					30		
Gly	Ser	Phe	Pro	Val	Pro	Ser	His	Arg	Cys	His	His	Lys	Gln	Lys	His
		35				40						45			
Cys	Pro	Pro	Thr	Leu	Ser	Gly	Gly	Gly	Leu	Pro	Ala	Thr	Pro	Leu	Leu
	50					55					60				
Phe	His	Pro	His	Thr	Lys	Gly	Ser	Gln	Ile	Leu	Met	Asp	Leu	Ser	His
65					70					75					80
Lys	Ala	Val	Lys	Arg	Gln	Ala	Ser	Phe	Cys	Asn	Ala	Ile	Thr	Phe	Ser
				85					90					95	
Asn	Arg	Pro	Val	Leu	Ile	Tyr	Glu	Gln	Val	Arg	Leu	Lys	Ile	Thr	Lys
			100					105					110		
Lys	Gln	Cys	Cys	Trp	Ser	Gly	Ala	Leu	Arg	Leu	Gly	Phe	Thr	Ser	Lys
		115				120						125			
Asp	Pro	Ser	Arg	Ile	His	Pro	Asp	Ser	Leu	Pro	Lys	Tyr	Ala	Cys	Pro
	130					135					140				
Asp	Leu	Val	Ser	Gln	Ser	Gly	Phe	Trp	Ala	Lys	Ala	Leu	Pro	Glu	Glu
145					150					155					160
Phe	Ala	Asn	Glu	Gly	Asn	Ile	Ile	Ala	Phe	Trp	Val	Asp	Lys	Lys	Gly
				165					170					175	
Arg	Val	Phe	Tyr	Arg	Ile	Asn	Glu	Ser	Ala	Ala	Met	Leu	Phe	Phe	Ser
			180					185					190		
Gly	Val	Arg	Thr	Val	Asp	Pro	Leu	Trp	Ala	Leu	Val	Asp	Val	Tyr	Gly
	195					200						205			
Leu	Thr	Arg	Gly	Val	Gln	Leu	Leu	Asp	Ser	Glu	Leu	Val	Leu	Pro	Glu
	210					215					220				
Ser	Pro	Val	Thr	Pro	Gly	Leu	Gly	Gln	Trp	Ser	Asp	Glu	Cys	Thr	Ile
225					230					235					240
Cys	Tyr	Glu	His	Ala	Val	Asp	Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met
				245					250					255	
Cys	Leu	Cys	Tyr	Ser	Cys	Gly	Leu	Arg	Leu	Lys	Lys	Ala	Leu	His	Ala
			260					265					270		
Cys	Cys	Pro	Ile	Cys	Arg	Arg	Pro	Ile	Lys	Asp	Ile	Ile	Lys	Thr	Tyr
		275					280					285			
Arg	Ser	Ser													
		290													

<210> 15
 <211> 1725
 <212> DNA
 <213> rat

<400> 15

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<212> DNA

<213> rat

<400> 17

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cgatgccatc acaagcagaa gcattgcccg cccgcgtgt caggtggggg gctcccggcc 180
acaccgctgc ttttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240
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ctcatctacg agcaagtcag gctgaagatc accaagaagc agtgcgtctg gagcggggcc 360
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<210> 18

<211> 344

<212> PRT

<213> rat

<400> 18

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 1           5           10           15
Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Asp Ser Ile Gly
 20           25           30
Ser Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His
 35           40           45
Cys Pro Pro Ala Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu
 50           55           60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His
 65           70           75           80
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser
 85           90           95
Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys
100           105           110
Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys
115           120           125
Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro
130           135           140
Asp Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu
145           150           155           160
Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly
165           170           175
Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser
180           185           190
Gly Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly
195           200           205
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Leu Thr Arg Gly Val Gln Leu Leu Gly Ser Thr Ile Met Ala Glu Arg
 210 215 220
 Gly Gly Pro Ser Leu Pro Cys Ser Pro Ala Ser Thr Pro Thr Ser Pro
 225 230 235 240
 Ser Ala Leu Gly Ser Arg Leu Ser Asp Pro Leu Leu Ser Thr Cys Gly
 245 250 255
 Ser Gly Pro Leu Gly Gly Ser Val Gly Gly Thr Ala Pro Asn Ser Pro
 260 265 270
 Val Ser Leu Pro Glu Ser Pro Val Thr Pro Gly Leu Gly Gln Trp Ser
 275 280 285
 Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val Asp Thr Val Ile Tyr
 290 295 300
 Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys
 305 310 315 320
 Lys Ala Leu His Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp
 325 330 335
 Ile Ile Lys Thr Tyr Arg Ser Ser
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<210> 19
 <211> 888
 <212> DNA
 <213> rat

<400> 19
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 cggggccacc cccagaacct caaagactcc atcgggagct ccttcccgtt cccctctcac 120
 cgatgccatc acaagcagaa gcattgcccg cccgcgtgt caggtggggg gctcccgcc 180
 acaccgctgc tcttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240
 aaggccgtca agaggcaggc cagcttctgt aatgccatca ccttcagcaa ccgccccgtc 300
 ctcatctacg agcaagtcag gctgaagatc accaagaagc agtgctgctg gagcggggcc 360
 ctgcgacttg gcttcaccag caaggaccct tccgcaccc accccgactc actgcccagg 420
 tacgcctgcc ctgacctggt gtcccagagt ggcttctggg ccaaagcgtt gcctgaggag 480
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 cggatcaatg agtcggctgc catgctgttc ttcagcgggg ttcgaacggc ggacccgctc 600
 tgggccctgg tggacgtcta tggcctcaca cggggtgtcc agctgctagg aacagcccc 660
 aactcacctg tgagcctgcc cgagtcacca gtgaccccg gtctggggcca gtggagcgat 720
 gaatgcacca tttgctatga acacgcagt gatacagtca tctacacgtg tggccacatg 780
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<210> 20
 <211> 295
 <212> PRT
 <213> rat

<400> 20
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 1 5 10 15
 Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Asp Ser Ile Gly
 20 25 30
 Ser Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His
 35 40 45
 Cys Pro Pro Ala Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu

50		55		60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His				
65		70		75
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser				
	85		90	
Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys				
	100		105	110
Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys				
	115		120	125
Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro				
	130		135	140
Asp Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu				
145		150		155
Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly				
	165		170	175
Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser				
	180		185	190
Gly Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly				
	195		200	205
Leu Thr Arg Gly Val Gln Leu Leu Gly Thr Ala Pro Asn Ser Pro Val				
	210		215	220
Ser Leu Pro Glu Ser Pro Val Thr Pro Gly Leu Gly Gln Trp Ser Asp				
225		230		235
Glu Cys Thr Ile Cys Tyr Glu His Ala Val Asp Thr Val Ile Tyr Thr				
	245		250	255
Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys Lys				
	260		265	270
Ala Leu His Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Ile				
	275		280	285
Ile Lys Thr Tyr Arg Ser Ser				
290		295		

<210> 21

<211> 1675

<212> DNA

<213> Homo sapien

<400> 21

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ttccacgcgc aggccaaagg caagaacgtg cggctggacg gccactcgcg ccggggccaca 180
cggcgcaaca gcttctgcaa tggcgctcacg ttcacgcagc ggcccatccg gctgtacgag 240
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gcggccaact tcgacaacaa cgagctcgag aacaaccagg tgggtggcaa gctggggccac 720
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gagagcctct tcgtggaggt gggccgtccg gggctggcgg cggccggcgc gctggccttc 1020
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gcgctgctcg accgcaaaga gtactgggtg gtggcgcgcg ccggggcccgt gccgagcggc 1140
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cgtccgcgcg gccgcctget gtgcgtcgac accacgcagg cgctctgggc cttcttcgcc 1260
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atgtgcctgt gccacagctg cggcctgcgg ctcaagcgac agggccgggc ctgctgcccc 1620
atctgccggc ggcccatcaa ggacgtcatt aagatctaca ggccatagcc tagcc 1675

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<210> 22

<211> 555

<212> PRT

<213> Homo sapien

<400> 22

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Met Gly Asn Thr Val His Arg Thr Leu Pro Asp Pro Ser Pro Pro Ala
  1          5          10          15
Arg Leu Leu Ala Thr Arg Pro Cys Cys Gly Pro Gly Pro Glu Arg Arg
      20          25          30
Pro Val Leu Gly Glu Ala Pro Arg Phe His Ala Gln Ala Lys Gly Lys
      35          40          45
Asn Val Arg Leu Asp Gly His Ser Arg Arg Ala Thr Arg Arg Asn Ser
      50          55          60
Phe Cys Asn Gly Val Thr Phe Thr Gln Arg Pro Ile Arg Leu Tyr Glu
      65          70          75          80
Gln Val Arg Leu Arg Leu Val Ala Val Arg Pro Gly Trp Ser Gly Ala
      85          90          95
Leu Arg Phe Gly Phe Thr Ala His Asp Pro Ser Leu Met Ser Ala Gln
      100          105          110
Asp Ile Pro Lys Tyr Ala Cys Pro Asp Leu Val Thr Arg Pro Gly Tyr
      115          120          125
Trp Ala Lys Ala Leu Pro Glu Asn Leu Ala Leu Arg Asp Thr Val Leu
      130          135          140
Ala Tyr Trp Ala Asp Arg His Gly Arg Val Phe Tyr Ser Val Asn Asp
      145          150          155          160
Gly Glu Pro Val Leu Phe His Cys Gly Val Ala Val Gly Gly Pro Leu
      165          170          175
Trp Ala Leu Ile Asp Val Tyr Gly Ile Thr Asp Glu Val Gln Leu Leu
      180          185          190
Glu Ser Ala Phe Ala Asp Thr Leu Thr Pro Ala Arg Leu Ser Gln Ala
      195          200          205
Arg Phe Ser Ala Cys Leu Pro Pro Ser Ser His Asp Ala Ala Asn Phe
      210          215          220
Asp Asn Asn Glu Leu Glu Asn Asn Gln Val Val Ala Lys Leu Gly His
      225          230          235          240
Leu Ala Leu Gly Arg Ala Pro Gly Pro Pro Pro Ala Asp Ala Ala Ala
      245          250          255
Ala Ala Ile Pro Cys Gly Pro Arg Glu Arg Pro Arg Pro Ala Ser Ser
      260          265          270
Pro Ala Leu Leu Glu Ala Asp Leu Arg Phe His Ala Thr Arg Gly Pro
      275          280          285

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Asp	Val	Ser	Leu	Ser	Ala	Asp	Arg	Lys	Val	Ala	Cys	Ala	Pro	Arg	Pro
290						295					300				
Asp	Gly	Gly	Arg	Thr	Leu	Val	Phe	Ser	Glu	Arg	Pro	Leu	Arg	Pro	Gly
305					310					315					320
Glu	Ser	Leu	Phe	Val	Glu	Val	Gly	Arg	Pro	Gly	Leu	Ala	Ala	Pro	Gly
				325					330					335	
Ala	Leu	Ala	Phe	Gly	Ile	Thr	Ser	Cys	Asp	Pro	Gly	Val	Leu	Arg	Pro
			340					345					350		
Asn	Glu	Leu	Pro	Ala	Asp	Pro	Asp	Ala	Leu	Leu	Asp	Arg	Lys	Glu	Tyr
		355					360					365			
Trp	Val	Val	Ala	Arg	Ala	Gly	Pro	Val	Pro	Ser	Gly	Gly	Asp	Ala	Leu
	370					375					380				
Ser	Phe	Thr	Leu	Arg	Pro	Gly	Gly	Asp	Val	Leu	Leu	Gly	Ile	Asn	Gly
385					390					395					400
Arg	Pro	Arg	Gly	Arg	Leu	Leu	Cys	Val	Asp	Thr	Thr	Gln	Ala	Leu	Trp
				405					410					415	
Ala	Phe	Phe	Ala	Val	Arg	Gly	Gly	Val	Ala	Gly	Gln	Leu	Arg	Leu	Leu
			420					425					430		
Gly	Thr	Leu	Gln	Ser	Ser	Pro	Ala	Thr	Thr	Thr	Pro	Ser	Gly	Ser	Leu
		435					440					445			
Ser	Gly	Ser	Gln	Asp	Asp	Ser	Asp	Ser	Asp	Met	Thr	Phe	Ser	Val	Asn
	450					455					460				
Gln	Ser	Ser	Ser	Ala	Ser	Glu	Ser	Ser	Leu	Val	Thr	Ala	Pro	Ser	Ser
465					470					475					480
Pro	Leu	Ser	Pro	Pro	Val	Ser	Pro	Val	Phe	Ser	Pro	Pro	Glu	Pro	Ala
				485					490					495	
Gly	Ile	Lys	Asn	Gly	Glu	Cys	Thr	Val	Cys	Phe	Asp	Gly	Glu	Val	Asp
			500					505					510		
Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met	Cys	Leu	Cys	His	Ser	Cys	Gly
		515				520						525			
Leu	Arg	Leu	Lys	Arg	Gln	Ala	Arg	Ala	Cys	Cys	Pro	Ile	Cys	Arg	Arg
	530					535					540				
Pro	Ile	Lys	Asp	Val	Ile	Lys	Ile	Tyr	Arg	Pro					
545					550					555					

<210> 23
 <211> 1129
 <212> DNA
 <213> Homo sapien

<400> 23
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 aacttcgaca acaacgagct cgagaacaac caggtggtgg ccaagctggg ccacctggcg 180
 ctggggccgcg ccccgggccc accgccagcc gacgccgcgg ccgccgccat tccgtgcggg 240
 ccccgctgagc gcccgcgccc cgcgctcgctg ccggcgctac tggaggccga cctgcgcttc 300
 cacgcaacac gcggggccga cgtgagcctg tcggccgacc gcaaagtggc ctgcgcaccg 360
 cggccccagc gcggccgcac gctggtcttc tccgagcgcc cgctgcggcc cggcgagagc 420
 ctcttcgtgg aggtggggcg tccggggctg gcggcgcccc gcgcgctggc cttcggcatc 480
 acgtcgtgcg acccgggcgt gctacggccc aacgagctgc ccgccgacc agacgcgctg 540
 ctcgaccgca aagagtactg ggtggtggcg cgcgccgggc ccgtgccgag cggcggcgac 600
 gcgctcagct tcacgctgcg gcccggcggc gacgtgctcc tgggcatcaa cgggcgctcc 660
 cgcggccgcc tgctgtgcgt cgacaccacg caggcgctct gggccttctt cgccgtgcgc 720
 ggccggcgctc cgggccagct gcgtctcttc ggtaccctgc agtccagccc tgcgaccacg 780

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tgcacgggtgt gcttcgatgg cgaggtggac acggtcactt acacgtgtgg acacatgtgc 1020
ctgtgccaca gctgcggcct gcgggtcaag cgacaggccc gggcctgctg ccccatctgc 1080
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<210> 24

<211> 373

<212> PRT

<213> Homo sapien

<400> 24

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Met Gly Asn Thr Val His Arg Thr Leu Pro Glu Ser Ala Phe Ala Asp
 1          5          10          15
Thr Leu Thr Pro Ala Arg Leu Ser Gln Ala Arg Phe Ser Ala Cys Leu
 20          25          30
Pro Pro Ser Ser His Asp Ala Ala Asn Phe Asp Asn Asn Glu Leu Glu
 35          40          45
Asn Asn Gln Val Val Ala Lys Leu Gly His Leu Ala Leu Gly Arg Ala
 50          55          60
Pro Gly Pro Pro Pro Ala Asp Ala Ala Ala Ala Ile Pro Cys Gly
 65          70          75          80
Pro Arg Glu Arg Pro Arg Pro Ala Ser Ser Pro Ala Leu Leu Glu Ala
 85          90          95
Asp Leu Arg Phe His Ala Thr Arg Gly Pro Asp Val Ser Leu Ser Ala
 100          105          110
Asp Arg Lys Val Ala Cys Ala Pro Arg Pro Asp Gly Gly Arg Thr Leu
 115          120          125
Val Phe Ser Glu Arg Pro Leu Arg Pro Gly Glu Ser Leu Phe Val Glu
 130          135          140
Val Gly Arg Pro Gly Leu Ala Ala Pro Gly Ala Leu Ala Phe Gly Ile
 145          150          155          160
Thr Ser Cys Asp Pro Gly Val Leu Arg Pro Asn Glu Leu Pro Ala Asp
 165          170          175
Pro Asp Ala Leu Leu Asp Arg Lys Glu Tyr Trp Val Val Ala Arg Ala
 180          185          190
Gly Pro Val Pro Ser Gly Gly Asp Ala Leu Ser Phe Thr Leu Arg Pro
 195          200          205
Gly Gly Asp Val Leu Leu Gly Ile Asn Gly Arg Pro Arg Gly Arg Leu
 210          215          220
Leu Cys Val Asp Thr Thr Gln Ala Leu Trp Ala Phe Phe Ala Val Arg
 225          230          235          240
Gly Gly Val Ala Gly Gln Leu Arg Leu Leu Gly Thr Leu Gln Ser Ser
 245          250          255
Pro Ala Thr Thr Thr Pro Ser Gly Ser Leu Ser Gly Ser Gln Asp Asp
 260          265          270
Ser Asp Ser Asp Met Thr Phe Ser Val Asn Gln Ser Ser Ser Ala Ser
 275          280          285
Glu Ser Ser Leu Val Thr Ala Pro Ser Ser Pro Leu Ser Pro Pro Val
 290          295          300
Ser Pro Val Phe Ser Pro Pro Glu Pro Ala Gly Ile Lys Asn Gly Glu
 305          310          315          320
Cys Thr Val Cys Phe Asp Gly Glu Val Asp Thr Val Ile Tyr Thr Cys
 325          330          335

```

Gly His Met Cys Leu Cys His Ser Cys Gly Leu Arg Leu Lys Arg Gln
 340 345 350
 Ala Arg Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Val Ile
 355 360 365
 Lys Ile Tyr Arg Pro
 370

<210> 25
 <211> 955
 <212> DNA
 <213> Homo sapien

<400> 25
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 ttccacgcgc aggccaaagg caagaacgtg cggctggacg gccactcgcg ccggggccaca 180
 cggcgcaaca gcttctgcaa tggcgctcag ttacgcagc ggcccatccg gctgtacgag 240
 caggtgcggc tgcgcctggt ggccgtgcgc cctggctgga gcggcgcgct gcgcttcggc 300
 ttaccgcgc acgatccgtc gctcatgagc gcccaggaca tccccaaagta cgcttgcgcc 360
 gacctggtca cgcggcgccg ctactggggc aaggcactgc ccgagaacct ggcgctgcgc 420
 gacacggtgc tggcctaactg ggccgaccgc cacggccgcg tgttctacag cgtgaacgac 480
 ggcgagccgg tgcctttcca ctgcggcgctg gccgtgggcg gcccgctctg ggcgctcatt 540
 gatgtctacg gcatcaccga cgaggtgcag cttctgggta ccctgcagtc cagccctgcg 600
 accacgactc catcagggtc cctcagcggc tcccaggacg atagtgattc agatatgacc 660
 ttcatgttca accagtcttc ctgcgcatct gagtcatccc tggtgacggc cccagctcc 720
 ccgtgagcc ccccggtgtc ccccggtgtc tccccaccgg agccggcagg catcaagaat 780
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 atctgcggc ggcccatcaa ggacgtcatt aagatctaca ggccatagcc tagcc 955

<210> 26
 <211> 315
 <212> PRT
 <213> Homo sapien

<400> 26
 Met Gly Asn Thr Val His Arg Thr Leu Pro Asp Pro Ser Pro Pro Ala
 1 5 10 15
 Arg Leu Leu Ala Thr Arg Pro Cys Cys Gly Pro Gly Pro Glu Arg Arg
 20 25 30
 Pro Val Leu Gly Glu Ala Pro Arg Phe His Ala Gln Ala Lys Gly Lys
 35 40 45
 Asn Val Arg Leu Asp Gly His Ser Arg Arg Ala Thr Arg Arg Asn Ser
 50 55 60
 Phe Cys Asn Gly Val Thr Phe Thr Gln Arg Pro Ile Arg Leu Tyr Glu
 65 70 75 80
 Gln Val Arg Leu Arg Leu Val Ala Val Arg Pro Gly Trp Ser Gly Ala
 85 90 95
 Leu Arg Phe Gly Phe Thr Ala His Asp Pro Ser Leu Met Ser Ala Gln
 100 105 110
 Asp Ile Pro Lys Tyr Ala Cys Pro Asp Leu Val Thr Arg Pro Gly Tyr
 115 120 125
 Trp Ala Lys Ala Leu Pro Glu Asn Leu Ala Leu Arg Asp Thr Val Leu
 130 135 140

Ala	Tyr	Trp	Ala	Asp	Arg	His	Gly	Arg	Val	Phe	Tyr	Ser	Val	Asn	Asp
145					150					155					160
Gly	Glu	Pro	Val	Leu	Phe	His	Cys	Gly	Val	Ala	Val	Gly	Gly	Pro	Leu
				165						170					175
Trp	Ala	Leu	Ile	Asp	Val	Tyr	Gly	Ile	Thr	Asp	Glu	Val	Gln	Leu	Leu
			180					185					190		
Gly	Thr	Leu	Gln	Ser	Ser	Pro	Ala	Thr	Thr	Thr	Pro	Ser	Gly	Ser	Leu
		195					200					205			
Ser	Gly	Ser	Gln	Asp	Asp	Ser	Asp	Ser	Asp	Met	Thr	Phe	Ser	Val	Asn
	210					215					220				
Gln	Ser	Ser	Ser	Ala	Ser	Glu	Ser	Ser	Leu	Val	Thr	Ala	Pro	Ser	Ser
225				230						235					240
Pro	Leu	Ser	Pro	Pro	Val	Ser	Pro	Val	Phe	Ser	Pro	Pro	Glu	Pro	Ala
				245					250					255	
Gly	Ile	Lys	Asn	Gly	Glu	Cys	Thr	Val	Cys	Phe	Asp	Gly	Glu	Val	Asp
			260					265					270		
Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met	Cys	Leu	Cys	His	Ser	Cys	Gly
		275					280					285			
Leu	Arg	Leu	Lys	Arg	Gln	Ala	Arg	Ala	Cys	Cys	Pro	Ile	Cys	Arg	Arg
	290					295					300				
Pro	Ile	Lys	Asp	Val	Ile	Lys	Ile	Tyr	Arg	Pro					
305					310					315					

<210> 27
 <211> 1641
 <212> DNA
 <213> Rat

<400> 27
 atgggcaaca cgggtgcaccg gaccctgccg gactccagcc ctctctgcacg cctcctggcc 60
 acccgccctt gctacggccc gggcccggag aggcgagcgg tcctggggcga ggcgccacgc 120
 ttccacgcgc aggccaaagg caagaacgtg cgtctagacg gtcactcgcg caggggccacg 180
 cgacggaaca gcttctgcaa cggagtcacc ttcacgcagc ggcccattcg cctgtacgag 240
 cagggtgcggg tgcgcctggg ggctgtgctg cctggctgga gcggcgcgct gcgcttcggc 300
 ttcactgcgc acgacccgtc gctcatgagc gcacaggata tccccaaagta cgcttgcgcc 360
 gacctgggtca cagcacctgg atactggggc aaggcgtgc cggagaacct ggcgctgcgg 420
 gacacgggtgc tggcctactg ggctgatcgt cacggctcgc tcttctatag tgtctatgat 480
 ggcgaaccag tgctgttcca ctgcggcggtg gccgtgggaa gccactctg ggcactcatc 540
 gacgtctatg gcatcacgga cgaggtgcag ctgctggaaa gcacctgcgc agacacgctg 600
 acccgctgc gcctgggcca ggcgcgcctc agcgcctgcc cgcctccggg cagccacgat 660
 gctgccaaact tcgataataa cgagctggag aataaccagg tggtagccaa gctgggtcac 720
 ttggctctcg gcgctcggga cgcgcgcgtc ccgtgcgtgg cccgcgaacg cgcgaggccc 780
 gcttcttcac ccgcgttgct ggacgctgag ctgcgtttcc acgccacgcg cggccccgac 840
 gtgagcctgt ttgcggaccg caggttagct tgcgcgcccc gccccgacgg cggccgcacg 900
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 gtggtggcgc gcgcggggcc cgtgcccagc ggaggcgacg cactcagctt cacgctgcga 1140
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 tcagaatcgt ctctggtgac agcccccagc tccccactga gtccccagtc gtccccggcc 1440
 ttctctgcac ccgagccggc cggcagcagg aatggagagt gcacggtgtg cttcgacagc 1500

355	360	365
Pro Ser Gly Gly Asp Ala Leu Ser Phe Thr Leu Arg Pro Gly Gly Asp		
370	375	380
Val Leu Leu Ala Val Asn Gly Arg Pro Arg Gly Arg Leu Leu Cys Val		
385	390	395
Asp Thr Ser Gln Ala Leu Trp Ala Phe Phe Ala Val Arg Gly Gly Val		
405	410	415
Ala Gly Gln Leu Arg Leu Leu Gly Thr Val Gln Ser Gly Pro Glu Ala		
420	425	430
Thr Thr Pro Ser Gly Ser Phe Ser Gly Ser Gln Asp Asp Ser Asp Ser		
435	440	445
Asp Met Thr Phe Gly Val Asn Gln Ser Ser Ser Ala Ser Glu Ser Ser		
450	455	460
Leu Val Thr Ala Pro Ser Ser Pro Leu Ser Pro Pro Val Ser Pro Ala		
465	470	475
Phe Ser Ala Pro Glu Pro Ala Gly Ser Arg Asn Gly Glu Cys Thr Val		
485	490	495
Cys Phe Asp Ser Glu Val Asp Thr Val Ile Tyr Thr Cys Gly His Met		
500	505	510
Cys Leu Cys His Ser Cys Arg Leu Arg Leu Arg Lys Gln Ala Arg Ala		
515	520	525
Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Val Ile Lys Ile Tyr		
530	535	540
Arg Pro		
545		

<210> 29
 <211> 789
 <212> DNA
 <213> Homo sapien

<400> 29
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 cgcaccacgt tccacgacgg catcgtgttc agccagcggc cggcgcgcct gggcgagcgt 180
 gtggcgctgc gactgctgcg ggaggagagc ggctggctgc gcggcctccg cgtgggcttc 240
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 tgccggctcc tgetgctga gggcgtgccc gtcggcgccc cgctctgggc cgtgatggac 480
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 cccatgccat gggacctcag caacaaggct gtgcctgagc ccaaagccac accaggagag 600
 gagtgtgcca tctgcttcta tcacgtgcc aacaccgcc ttgtgccctg cggccacaca 660
 tacttctgca gatactgtgc ctggcggtc ttcagcgata cggccaagt ccctgtgtgc 720
 cgctggcaga tagaggcggg agccctgctg cagggccctc ctgctctgag gggtgaggaa 780
 ggctcatga 789

<210> 30
 <211> 262
 <212> PRT
 <213> Homo sapien

<400> 30
 Met Gly Ala Gln Leu Cys Phe Glu Ala Asn Ala Lys Ala Pro Arg Glu

<210> 32
 <211> 254
 <212> PRT
 <213> mouse

<400> 32

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Met Gly Ser Leu Leu Ser Pro Glu Ala Asn Ala Glu Val Pro Arg Glu
 1           5           10          15
Ala Leu Ser Phe His Gly Asn Ala Thr Gly Ala Gln Val His Leu Asp
 20          25          30
Asp Gln Arg Ser Thr Ala Arg Arg Arg Ser Thr Phe His Asp Gly Ile
 35          40          45
Val Phe Ser Gln Arg Pro Val Trp Pro Gly Glu Arg Val Ala Leu Arg
 50          55          60
Val Leu Arg His Glu Glu Gly Trp Cys Gly Gly Leu Arg Val Gly Phe
 65          70          75          80
Thr Arg Leu Asp Pro Ala Gln Val Ala Ala Ser Cys Leu Pro Pro Phe
 85          90          95
Val Cys Pro Asp Leu Glu Glu Gln Ser Pro Thr Trp Ala Ala Leu Leu
100         105         110
Pro Glu Gly Phe Val Arg Ala Gly Asn Val Val Cys Phe Trp Val Asn
115         120         125
Arg Arg Gly Trp Leu Phe Ala Lys Val Asn Ala Gly Arg Pro Leu Leu
130         135         140
Leu Arg Lys Asp Val Leu Val Gln Gly Ala Pro Leu Trp Ala Val Met
145         150         155         160
Asp Val Tyr Gly Thr Thr Lys Ala Ile Glu Leu Leu Asp Pro Lys Ala
165         170         175
Asn Ala Trp Ile Arg Ser Gly Glu Pro Val Pro Glu Ser Glu Val Ile
180         185         190
Ser Gly Glu Glu Cys Val Ile Cys Phe His Asn Thr Ala Asn Thr Arg
195         200         205
Leu Met Pro Cys Gly His Ser His Phe Cys Gly Ser Cys Ala Trp His
210         215         220
Ile Phe Lys Asp Thr Ala Arg Cys Pro Ile Cys Arg Trp Gln Ile Glu
225         230         235         240
Glu Val Ala Val Val Ser Ser Leu Lys Ala Glu Glu Gly Ser
245         250

```

<210> 33
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 33

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cgcttccatc ggggtgcacgg tgccaacatc cgcgtggacc cctctgggac gcgggccaca 60
cgcgtggaga gcttcgcca cggcgtgtgc ttcagccgag agccgctggc cccggggccag 120
gtcttcctgg tcgagatcga ggagaaagag ctgggctggg gcggacatct gcgtctcggg 180
ctgaccgcgc tggaccccg cagtctggcc cccgttcccg agttttctct gcccgatctg 240
gtcaacctgg                                     250

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<210> 34
 <211> 83
 <212> PRT

<213> Homo sapien

<400> 34

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Arg Phe His Arg Val His Gly Ala Asn Ile Arg Val Asp Pro Ser Gly
 1           5           10           15
Thr Arg Ala Thr Arg Val Glu Ser Phe Ala His Gly Val Cys Phe Ser
      20           25           30
Arg Glu Pro Leu Ala Pro Gly Gln Val Phe Leu Val Glu Ile Glu Glu
      35           40           45
Lys Glu Leu Gly Trp Cys Gly His Leu Arg Leu Gly Leu Thr Ala Leu
      50           55           60
Asp Pro Ala Ser Leu Ala Pro Val Pro Glu Phe Ser Leu Pro Asp Leu
65           70           75           80
Val Asn Leu
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<210> 35

<211> 1743

<212> DNA

<213> rat

<400> 35

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gtgttactgg gctttgctgg acggaataaa agtgggcgca agcatgacct cctgatgagg 120
gcgttgcaatt tactgaagag tggctgcagc cctgcggttc agattaaaat tcgagaatta 180
tacagacgcc gatacccacg gacacttgaa ggactttctg atctatccac aatcaaattct 240
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atccactcgt tgccttctac ttccattgca cctcattcac cgtcatctcc tgtcgttct 360
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cctgtccatc ctgacgtgca gttaaaaacg ctgcccttct atgacgtcct tgatgttctc 480
atcaagccca caagtttagt tcaaagcagt attcagcggg ttcaagagaa gttttttatt 540
tttgctttga cccccagca agttagagag atatgcattt caagggattt tttgccagg 600
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cctcaagaag ataactatcc caatagtttg tgtataaaag taaatgggaa actctttcct 720
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ctgaatatta catctttagt gagattgtct tcagctgtgc caaatcagat ttctatttct 840
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gtgtcgagca tgtcatcaga tttgccaggg ttggattttc tttcccttat tccagttgat 1680
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<210> 36

<211> 580

<212> PRT

<213> rat

<400> 36

Met Ala Asp Phe Glu Glu Leu Arg Asn Met Val Ser Ser Phe Arg Val
1 5 10 15
Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn Lys Ser Gly
20 25 30
Arg Lys His Asp Leu Leu Met Arg Ala Leu His Leu Leu Lys Ser Gly
35 40 45
Cys Ser Pro Ala Val Gln Ile Lys Ile Arg Glu Leu Tyr Arg Arg Arg
50 55 60
Tyr Pro Arg Thr Leu Glu Gly Leu Ser Asp Leu Ser Thr Ile Lys Ser
65 70 75 80
Ser Val Phe Ser Leu Asp Gly Ser Ser Ser Pro Val Glu Pro Asp Leu
85 90 95
Ala Val Ala Gly Ile His Ser Leu Pro Ser Thr Ser Ile Ala Pro His
100 105 110
Ser Pro Ser Ser Pro Val Ala Ser Val Leu Leu Gln Asp Thr Lys Pro
115 120 125
Thr Phe Glu Met Gln Gln Pro Ser Pro Pro Ile Pro Pro Val His Pro
130 135 140
Asp Val Gln Leu Lys Thr Leu Pro Phe Tyr Asp Val Leu Asp Val Leu
145 150 155 160
Ile Lys Pro Thr Ser Leu Val Gln Ser Ser Ile Gln Arg Phe Gln Glu
165 170 175
Lys Phe Phe Ile Phe Ala Leu Thr Pro Gln Gln Val Arg Glu Ile Cys
180 185 190
Ile Ser Arg Asp Phe Leu Pro Gly Gly Arg Arg Asp Tyr Thr Val Gln
195 200 205
Val Gln Leu Arg Leu Cys Leu Ala Glu Thr Ser Cys Pro Gln Glu Asp
210 215 220
Asn Tyr Pro Asn Ser Leu Cys Ile Lys Val Asn Gly Lys Leu Phe Pro
225 230 235 240
Leu Pro Gly Tyr Ala Pro Pro Pro Lys Asn Gly Ile Glu Gln Lys Arg
245 250 255
Pro Gly Arg Pro Leu Asn Ile Thr Ser Leu Val Arg Leu Ser Ser Ala
260 265 270
Val Pro Asn Gln Ile Ser Ile Ser Trp Ala Ser Glu Ile Gly Lys Asn
275 280 285
Tyr Ser Met Ser Val Tyr Leu Val Arg Gln Leu Thr Ser Ala Met Leu
290 295 300
Leu Gln Arg Leu Lys Met Lys Gly Ile Arg Asn Pro Asp His Ser Lys
305 310 315 320
Ala Leu Ile Lys Glu Lys Leu Thr Ala Asp Pro Asp Ser Glu Ile Ala
325 330 335
Thr Thr Ser Leu Arg Val Ser Leu Met Cys Pro Leu Gly Lys Met Arg
340 345 350
Leu Thr Ile Pro Cys Arg Ala Val Thr Cys Thr His Leu Gln Cys Phe
355 360 365
Asp Ala Ala Leu Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Ile
370 375 380
Cys Pro Val Cys Asp Lys Lys Ala Ala Tyr Glu Ser Leu Ile Leu Asp
385 390 395 400

Gly Leu Phe Met Glu Ile Leu Asn Asp Cys Ser Asp Val Asp Glu Ile
405 410 415
Lys Phe Gln Glu Asp Gly Ser Trp Cys Pro Met Arg Pro Lys Lys Glu
420 425 430
Ala Met Lys Val Thr Ser Gln Pro Cys Thr Lys Val Glu Ser Ser Ser
435 440 445
Val Phe Ser Lys Pro Cys Ser Val Thr Val Ala Ser Asp Ala Ser Lys
450 455 460
Lys Lys Ile Asp Val Ile Asp Leu Thr Ile Glu Ser Ser Ser Asp Glu
465 470 475 480
Glu Glu Asp Pro Pro Ala Lys Arg Lys Cys Ile Phe Met Ser Glu Thr
485 490 495
Gln Ser Ser Pro Thr Lys Gly Val Leu Met Tyr Gln Pro Ser Ser Val
500 505 510
Arg Val Pro Ser Val Thr Ser Val Asp Pro Ala Ala Ile Pro Pro Ser
515 520 525
Leu Thr Asp Tyr Ser Val Pro Phe His His Thr Pro Val Ser Ser Met
530 535 540
Ser Ser Asp Leu Pro Gly Leu Asp Phe Leu Ser Leu Ile Pro Val Asp
545 550 555 560
Pro Gln Ser His Leu Thr Leu Asn Ser Lys Gln Tyr Val Cys His His
565 570 575
His Gln Pro Pro
580

<210> 37
<211> 1251
<212> DNA
<213> Homo sapien

<400> 37
atgagcacca agcagatcac ttgcaggtat tttatgcatg gtgtgtgtcg ggaaggaagt 60
cagtgcctat tctcacatga cttggcaaac agcaaaccgt ccaccatctg caagtactac 120
cagaagggct actgtgccta tggaaactcg tgcagatatg accacacgag gccctctgct 180
gcagctggag gtgctgtggg caccatggcc cacagtgtgc cctccccagc tttccacagt 240
cctcaccctc cttccgaggt cactgcatcc attgtgaaaa ctaactcaca tgaaccgga 300
aagcgtgaaa agagaacatt ggttcttaga gaccgaaatc tctctggcat ggctgaaagg 360
aagaccgagc cgagcatggt gagtaatcca ggcagctgca gcgaccccca gccagcccc 420
gagatgaagc cgcattccta cctggatgcc atcaggagtg gccttgatga cgtggaggcc 480
agcagctcct acagcaacga gcagcagctg tgcccctacg cagctgctgg ggagtgccgg 540
tttggggatg cctgtgtcta cctgcacggg gaggtgtgtg aaatctgtag gctgcaagtc 600
ttgcacccat tcgacccaga gcagaggaag gctcatgaaa agatctgcat gttgacgttc 660
gaacacgaga tggaaaaggc ctttgccttc caggcaagcc aggacaaagt gtgcagtatc 720
tgcatggaag tgatcctgga gaaggcctct gcttctgaga ggagatttgg gattctctcc 780
aattgcaatc acacgtactg tttgtcctgc atccggcagt ggcggtgtgc cgaacagttt 840
gaaaacccaa tcattaagtc ttgtccagaa tgccgtgtga tatcagagtt tgtaattcca 900
agtgtgtatt ggggtggaaga tcagaataaa aagaacgagt tgattgaagc tttcaaacag 960
gggatgggga aaaaagcctg taaatacttt gagcaaggca aggggacctg cccatttggg 1020
agcaaatgtc tttatcgcca tgcttaccct gatgggcggc tagcagagcc tgagaaacct 1080
cggaacagc tcagttctca aggcactgtg aggttcttta attcagtgcg gctctgggat 1140
ttcatcgaga accgagaaag ccggcatgtc cccaacaatg aagatgtcga catgacagag 1200
ctcggggacc tcttcatgca ctttctgga gtggaatcat cagaacccta a 1251

<210> 38

<211> 416
 <212> PRT
 <213> Homo sapien

<400> 38

Met	Ser	Thr	Lys	Gln	Ile	Thr	Cys	Arg	Tyr	Phe	Met	His	Gly	Val	Cys	
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Arg	Glu	Gly	Ser	Gln	Cys	Leu	Phe	Ser	His	Asp	Leu	Ala	Asn	Ser	Lys	
			20					25					30			
Pro	Ser	Thr	Ile	Cys	Lys	Tyr	Tyr	Gln	Lys	Gly	Tyr	Cys	Ala	Tyr	Gly	
		35				40						45				
Thr	Arg	Cys	Arg	Tyr	Asp	His	Thr	Arg	Pro	Ser	Ala	Ala	Ala	Gly	Gly	
	50					55					60					
Ala	Val	Gly	Thr	Met	Ala	His	Ser	Val	Pro	Ser	Pro	Ala	Phe	His	Ser	
65					70					75					80	
Pro	His	Pro	Pro	Ser	Glu	Val	Thr	Ala	Ser	Ile	Val	Lys	Thr	Asn	Ser	
				85					90					95		
His	Glu	Pro	Gly	Lys	Arg	Glu	Lys	Arg	Thr	Leu	Val	Leu	Arg	Asp	Arg	
			100					105					110			
Asn	Leu	Ser	Gly	Met	Ala	Glu	Arg	Lys	Thr	Gln	Pro	Ser	Met	Val	Ser	
		115						120					125			
Asn	Pro	Gly	Ser	Cys	Ser	Asp	Pro	Gln	Pro	Ser	Pro	Glu	Met	Lys	Pro	
	130					135					140					
His	Ser	Tyr	Leu	Asp	Ala	Ile	Arg	Ser	Gly	Leu	Asp	Asp	Val	Glu	Ala	
145					150					155					160	
Ser	Ser	Ser	Tyr	Ser	Asn	Glu	Gln	Gln	Leu	Cys	Pro	Tyr	Ala	Ala	Ala	
				165					170					175		
Gly	Glu	Cys	Arg	Phe	Gly	Asp	Ala	Cys	Val	Tyr	Leu	His	Gly	Glu	Val	
			180					185					190			
Cys	Glu	Ile	Cys	Arg	Leu	Gln	Val	Leu	His	Pro	Phe	Asp	Pro	Glu	Gln	
		195				200						205				
Arg	Lys	Ala	His	Glu	Lys	Ile	Cys	Met	Leu	Thr	Phe	Glu	His	Glu	Met	
	210					215					220					
Glu	Lys	Ala	Phe	Ala	Phe	Gln	Ala	Ser	Gln	Asp	Lys	Val	Cys	Ser	Ile	
225					230					235					240	
Cys	Met	Glu	Val	Ile	Leu	Glu	Lys	Ala	Ser	Ala	Ser	Glu	Arg	Arg	Phe	
				245					250					255		
Gly	Ile	Leu	Ser	Asn	Cys	Asn	His	Thr	Tyr	Cys	Leu	Ser	Cys	Ile	Arg	
		260						265					270			
Gln	Trp	Arg	Cys	Ala	Glu	Gln	Phe	Glu	Asn	Pro	Ile	Ile	Lys	Ser	Cys	
		275					280						285			
Pro	Glu	Cys	Arg	Val	Ile	Ser	Glu	Phe	Val	Ile	Pro	Ser	Val	Tyr	Trp	
	290					295					300					
Val	Glu	Asp	Gln	Asn	Lys	Lys	Asn	Glu	Leu	Ile	Glu	Ala	Phe	Lys	Gln	
305					310					315					320	
Gly	Met	Gly	Lys	Lys	Ala	Cys	Lys	Tyr	Phe	Glu	Gln	Gly	Lys	Gly	Thr	
				325					330					335		
Cys	Pro	Phe	Gly	Ser	Lys	Cys	Leu	Tyr	Arg	His	Ala	Tyr	Pro	Asp	Gly	
		340						345					350			
Arg	Leu	Ala	Glu	Pro	Glu	Lys	Pro	Arg	Lys	Gln	Leu	Ser	Ser	Gln	Gly	
		355					360						365			
Thr	Val	Arg	Phe	Phe	Asn	Ser	Val	Arg	Leu	Trp	Asp	Phe	Ile	Glu	Asn	
	370					375					380					
Arg	Glu	Ser	Arg	His	Val	Pro	Asn	Asn	Glu	Asp	Val	Asp	Met	Thr	Glu	
385					390					395					400	

Leu Gly Asp Leu Phe Met His Leu Ser Gly Val Glu Ser Ser Glu Pro
 405 410 415

<210> 39
 <211> 738
 <212> DNA
 <213> Homo sapien

<400> 39
 atgaaacgga ggaagcaaga tgaagggcag agggaaggct cctgcatggc tgaggatgat 60
 gctgtggaca tcgagcatga gaacaacaac cgctttgagg agtatgagtg gtgtggacag 120
 aagcggatac gggccaccac tctcctggaa ggtggcttcc gaggtctctgg cttcatcatg 180
 tgcagcggca aagagaaccc ggacagtgat gctgacttgg atgtggatgg ggatgacact 240
 ctggagtatg ggaagccaca atacacagag gctgatgtca tcccctgcac aggcgaggag 300
 cctggtgaag ccaaggagag agaggcactt cggggcgcag tcctaaatgg cggccctccc 360
 agcacgcgca tcacacctga gttctctaaa tggggccagt atgagatgcc atccaccagc 420
 aatggtgaaa gcagcaagca ggaggccatg cagaagacct gcaagaacag cgacatcgag 480
 aaaatcaccg aagattcagc tgtgaccacg tttgaggctc tgaaggctcg ggtcagagaa 540
 cttgaacggc agctatctcg tggggaccgt taaaaatgcc tcatctgcat ggactcgtac 600
 tcgatgcccc taacgtccat ccagtgttgg cacgtgcact gcgaggagtg ctggctgctg 660
 accctgggtg ccaagaagct ctgccctcag tgcaacacga tcacagcgcc cggagacctg 720
 cggaggatct acttgtga 738

<210> 40
 <211> 245
 <212> PRT
 <213> Homo sapien

<400> 40
 Met Lys Arg Arg Lys Gln Asp Glu Gly Gln Arg Glu Gly Ser Cys Met
 1 5 10 15
 Ala Glu Asp Asp Ala Val Asp Ile Glu His Glu Asn Asn Asn Arg Phe
 20 25 30
 Glu Glu Tyr Glu Trp Cys Gly Gln Lys Arg Ile Arg Ala Thr Thr Leu
 35 40 45
 Leu Glu Gly Gly Phe Arg Gly Ser Gly Phe Ile Met Cys Ser Gly Lys
 50 55 60
 Glu Asn Pro Asp Ser Asp Ala Asp Leu Asp Val Asp Gly Asp Asp Thr
 65 70 75 80
 Leu Glu Tyr Gly Lys Pro Gln Tyr Thr Glu Ala Asp Val Ile Pro Cys
 85 90 95
 Thr Gly Glu Glu Pro Gly Glu Ala Lys Glu Arg Glu Ala Leu Arg Gly
 100 105 110
 Ala Val Leu Asn Gly Gly Pro Pro Ser Thr Arg Ile Thr Pro Glu Phe
 115 120 125
 Ser Lys Trp Ala Ser Asp Glu Met Pro Ser Thr Ser Asn Gly Glu Ser
 130 135 140
 Ser Lys Gln Glu Ala Met Gln Lys Thr Cys Lys Asn Ser Asp Ile Glu
 145 150 155 160
 Lys Ile Thr Glu Asp Ser Ala Val Thr Thr Phe Glu Ala Leu Lys Ala
 165 170 175
 Arg Val Arg Glu Leu Glu Arg Gln Leu Ser Arg Gly Asp Arg Tyr Lys
 180 185 190
 Cys Leu Ile Cys Met Asp Ser Tyr Ser Met Pro Leu Thr Ser Ile Gln

195	200	205
Cys Trp His Val His Cys Glu Glu Cys Trp Leu Arg Thr Leu Gly Ala		
210	215	220
Lys Lys Leu Cys Pro Gln Cys Asn Thr Ile Thr Ala Pro Gly Asp Leu		
225	230	235
Arg Arg Ile Tyr Leu		240
245		

<210> 41
 <211> 1425
 <212> DNA
 <213> Homo sapien

<400> 41
 atgtcgtcag aagatcgaga agctcaggag gatgaattgc tggccctggc aagtattttac 60
 gatggagatg aatttagaaa agcagagtct gtccaagggt gagaaaccag gatctatttg 120
 gatttgccac agaatttcaa gatatttgtg agcggcaatt caaatgagtg tctccagaat 180
 agtggtcttg aatacaccat ttgctttctg cctccacttg tgctgaactt tgaactgcc 240
 ccagattatc catcctcttc ccacacttca ttcacactta gtggcaaatg gctgtcacca 300
 actcagctat ctgctctatg caagcactta gacaacctat gggaagaaca ccgtggcagc 360
 gtggtcctgt ttgcttggtat gcaatttctt aaggaagaga ccctagcata cttgaatatt 420
 gtctctcctt ttgagctcaa gattgggttct cagaaaaaag tgcagagaag gacagctcaa 480
 gcttctccca acacagagct agattttgga ggagctgctg gatctgatgt agaccaagag 540
 gaaattgtgg atgagagagc agtgcaggat gtggaatcac tgtcaaatct gatccaggaa 600
 atcttggact ttgatcaagc tcagcagata aaatgcttta atagtaaatt gttcctgtgc 660
 agtatctgtt tctgtgagaa gctgggtagt gaatgcatgt acttcttggg gtgcaggcat 720
 gtgtactgca aagcctgtct gaaggactac tttgaaatcc agatcagaga tggccagggt 780
 caatgcctca actgccaga accaaagtgc cttcgggtgg ccactcctgg tcagggtcaa 840
 gagttagtgg aagcagagtt atttgcccggt tatgaccgcc ttctcctcca gtcctccttg 900
 gacctgatgg cagatgtggt gtactgcccc cggcctgctg gccagctgcc tgtgatgcag 960
 gaacctggct gcaccatggg tatctgctcc agctgcaatt ttgccttctg tactttgtgc 1020
 aggttgacct accatgggggt ctccccatgt aaggtgactg cagagaaatt aatggactta 1080
 cgaaatgaat acctgcaagc ggatgaggct aataaaagac ttttggatca aaggtatggt 1140
 aagagagtga ttcagaaggc actggaagag atggaaagta aggagtggct agagaagaac 1200
 tcaaagagct gcccatgttg tggaaactccc atagagaaat tagacggatg taacaagatg 1260
 acatgtactg gctgtatgca atatttctgt tggatttgca tgggttctct ctctagagca 1320
 aacccttaca aacatttcaa tgacctgggt tcaccatgtt ttaaccggct gttttatgct 1380
 gtggatgttg acgacgatat ttgggaagat gaggtagaag actag 1425

<210> 42
 <211> 474
 <212> PRT
 <213> Homo sapien

<400> 42
 Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
 1 5 10 15
 Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
 20 25 30
 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
 35 40 45
 Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
 50 55 60
 Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro

65	Pro	Asp	Tyr	Pro	Ser	Ser	Ser	Pro	Pro	Ser	Phe	Thr	Leu	Ser	Gly	Lys	80
					85					90					95		
Trp	Leu	Ser	Pro	Thr	Gln	Leu	Ser	Ala	Leu	Cys	Lys	His	Leu	Asp	Asn		
			100					105					110				
Leu	Trp	Glu	Glu	His	Arg	Gly	Ser	Val	Val	Leu	Phe	Ala	Trp	Met	Gln		
		115					120					125					
Phe	Leu	Lys	Glu	Glu	Thr	Leu	Ala	Tyr	Leu	Asn	Ile	Val	Ser	Pro	Phe		
	130					135					140						
Glu	Leu	Lys	Ile	Gly	Ser	Gln	Lys	Lys	Val	Gln	Arg	Arg	Thr	Ala	Gln		
145					150					155					160		
Ala	Ser	Pro	Asn	Thr	Glu	Leu	Asp	Phe	Gly	Gly	Ala	Ala	Gly	Ser	Asp		
			165						170					175			
Val	Asp	Gln	Glu	Glu	Ile	Val	Asp	Glu	Arg	Ala	Val	Gln	Asp	Val	Glu		
		180					185					190					
Ser	Leu	Ser	Asn	Leu	Ile	Gln	Glu	Ile	Leu	Asp	Phe	Asp	Gln	Ala	Gln		
	195					200					205						
Gln	Ile	Lys	Cys	Phe	Asn	Ser	Lys	Leu	Phe	Leu	Cys	Ser	Ile	Cys	Phe		
	210					215					220						
Cys	Glu	Lys	Leu	Gly	Ser	Glu	Cys	Met	Tyr	Phe	Leu	Glu	Cys	Arg	His		
225					230					235					240		
Val	Tyr	Cys	Lys	Ala	Cys	Leu	Lys	Asp	Tyr	Phe	Glu	Ile	Gln	Ile	Arg		
			245						250					255			
Asp	Gly	Gln	Val	Gln	Cys	Leu	Asn	Cys	Pro	Glu	Pro	Lys	Cys	Pro	Ser		
		260					265						270				
Val	Ala	Thr	Pro	Gly	Gln	Val	Lys	Glu	Leu	Val	Glu	Ala	Glu	Leu	Phe		
	275					280					285						
Ala	Arg	Tyr	Asp	Arg	Leu	Leu	Leu	Gln	Ser	Ser	Leu	Asp	Leu	Met	Ala		
	290				295					300							
Asp	Val	Val	Tyr	Cys	Pro	Arg	Pro	Cys	Cys	Gln	Leu	Pro	Val	Met	Gln		
305					310					315					320		
Glu	Pro	Gly	Cys	Thr	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe		
			325						330					335			
Cys	Thr	Leu	Cys	Arg	Leu	Thr	Tyr	His	Gly	Val	Ser	Pro	Cys	Lys	Val		
		340					345					350					
Thr	Ala	Glu	Lys	Leu	Met	Asp	Leu	Arg	Asn	Glu	Tyr	Leu	Gln	Ala	Asp		
	355					360						365					
Glu	Ala	Asn	Lys	Arg	Leu	Leu	Asp	Gln	Arg	Tyr	Gly	Lys	Arg	Val	Ile		
	370				375					380							
Gln	Lys	Ala	Leu	Glu	Glu	Met	Glu	Ser	Lys	Glu	Trp	Leu	Glu	Lys	Asn		
385					390					395					400		
Ser	Lys	Ser	Cys	Pro	Cys	Cys	Gly	Thr	Pro	Ile	Glu	Lys	Leu	Asp	Gly		
			405						410					415			
Cys	Asn	Lys	Met	Thr	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile		
		420					425					430					
Cys	Met	Gly	Ser	Leu	Ser	Arg	Ala	Asn	Pro	Tyr	Lys	His	Phe	Asn	Asp		
	435					440					445						
Pro	Gly	Ser	Pro	Cys	Phe	Asn	Arg	Leu	Phe	Tyr	Ala	Val	Asp	Val	Asp		
	450				455						460						
Asp	Asp	Ile	Trp	Glu	Asp	Glu	Val	Glu	Asp								
465					470												

<210> 43

<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> nuclear localization signal

<400> 43
His Lys Ala Val Lys Arg
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> nuclear localization signal

<400> 44
Arg Leu Lys Ile Thr Lys Lys
1 5

<210> 45
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> putative protein kinase phosphorylation site

<400> 45
Arg Pro Arg Ser Phe Thr
1 5

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> protein kinase phosphorylation site consensus
sequence

<221> VARIANT
<222> 2, 4, 5
<223> Xaa = any amino acid

<400> 46
Arg Xaa Arg Xaa Xaa Ser Thr
1 5

<210> 47
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 3, 5, 8, 10, 12, 15, 16, 17, 19, 20, 21, 22
<223> Xaa = any amino acid

<400> 47
Ser Thr Xaa Pro Xaa Ser Pro Xaa Ser Xaa Pro Xaa Ser Pro Xaa Xaa
1 5 10 15
Xaa Gly Xaa Xaa Xaa Xaa Ser Asp
20

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> neuralized homology repeat domain

<400> 48
Leu Pro Lys Tyr Ala Cys Pro Asp Leu
1 5